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60. (Twice Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a plurality of signals corresponding to probe intensities for a plurality of nucleic acid probes, each probe intensity indicating an extent of hybridization of a nucleic acid probe with at least one nucleic acid sequence including said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system comparing said plurality of probe intensities to each other; and

said computer system generating a base call identifying said unknown base according to results of said comparing step and said sequence of said nucleic acid probe.

61. The method of claim 60, wherein said comparing step includes the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

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62. (Twice Amended) The method of claim 61, wherein said generating step includes the step of identifying said unknown base when [according to] a nucleic acid probe having said higher probe intensity [if said] ratio is greater than a selected [predetermined] ratio value.

63. (Amended) The method of claim 62, wherein said selected [predetermined] ratio value is approximately 1.2.

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64. (Amended) The method of claim 60, further comprising the step of sorting said plurality of probe intensities by intensity before said comparing step.

65. The method of claim 60, wherein said at least one sequence includes a reference sequence.

66. The method of claim 65, wherein said comparing step includes the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to said probe hybridizing with said reference sequence.

67. The method of claim 65, wherein said comparing step includes the step of calculating first ratios of a wild-type probe intensity to each probe intensity of probes hybridizing with said reference sequence, wherein said wild-type probe intensity indicates an extent of hybridization of a complementary probe with said reference sequence.

68. The method of claim 67, wherein said comparing step includes the step of calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of probes hybridizing with said sample sequence.

69. The method of claim 68, wherein said comparing step includes the step of calculating third ratios of said first ratios to said second ratios.

70. (Amended) The method of claim 69, wherein said generating step includes the step of identifying said unknown base according to a base of said probe associated with a highest third ratio.

71. The method of claim 68, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity of a probe hybridizing with said reference sequence to a highest intensity of a probe hybridizing with said sample sequence.

72. --CANCELED--

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73. The method of claim 65, wherein probe intensities of probes hybridizing with said reference sequence are from a plurality of experiments.

74. The method of claim 73, wherein said comparing step includes the step of said computer system comparing probe intensities of probes hybridizing with said sample sequence to statistics about said plurality of experiments.

75. The method of claim 74, wherein said statistics include a mean and standard deviation.

76. The method of claim 73, further comprising the step of normalizing said plurality of probe intensities by dividing each probe intensity by a sum of related probe intensities, wherein related probe intensities are from probes that differ by a single base.

77. The method of claim 60, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

78. The method of claim 60, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

79. The method of claim 60, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

80. The method of claim 60, wherein said unknown base is identified as being A, C, G, or T.

81. (Twice Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a plurality of ~~signals corresponding to~~ probe intensities for a plurality of nucleic acid probes, each probe intensity indicating an extent of hybridization of a nucleic acid

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probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system calculating a ratio of a higher probe intensity to a lower probe intensity; and

said computer system generating a base call identifying said unknown base according to a base of a nucleic acid probe having said higher probe intensity if said ratio is greater than a predetermined ratio value.

82. The method of claim 81, wherein said predetermined ratio value is approximately 1.2.

83. (Amended) The method of claim 81, further comprising the step of sorting said plurality of probe intensities by intensity before said comparing step.

84. The method of claim 81, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

85. The method of claim 81, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

86. The method of claim 81, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

87. The method of claim 81, wherein said unknown base is identified as being A, C, G, or T.

88. (Twice Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

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inputting a first set of signals corresponding to a first set of probe intensities, each probe intensity in said first set indicating an extent of hybridization of a nucleic acid probe with a reference nucleic acid sequence, and each nucleic acid probe differing from each other by at least a single base;

inputting a second set of signals corresponding to a second set of probe intensities, each probe intensity in said second set indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system comparing at least one of said probe intensities in said first set and at least one of said probe intensities in said second set; and

said computer system generating a base call identifying said unknown base according to results of said comparing step and said sequences of said probes in said first and second sets.

89. The method of claim 88, wherein said comparing step includes the step of calculating first ratios of a wild-type probe intensity to each probe intensity of probes hybridizing with said reference sequence, wherein said wild-type probe intensity indicates an extent of hybridization of a complementary probe with said reference sequence.

90. The method of claim 89, wherein said comparing step includes the step of calculating second ratios of the highest probe intensity of probes hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

91. The method of claim 90, wherein said comparing step further includes the step of calculating third ratios of said first ratios to said second ratios.

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92. (Amended) The method of claim 91, wherein said generating step includes the step of identifying said unknown base according to a base of said probe associated with a highest third ratio.

93. The method of claim 88, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity in said first set to a highest intensity in said second set.

94. --CANCELED--

95. The method of claim 88, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

96. The method of claim 88, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

97. The method of claim 88, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

98. The method of claim 88, wherein said unknown base is identified as being A, C, G, or T.

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99. (Twice Amended) In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting ~~signals corresponding to~~ statistics about a plurality of experiments, each of said experiments producing probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid probe with a reference nucleic acid sequence, and each nucleic acid probe differing from each other by at least a single base;

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inputting a plurality of signals corresponding to probe intensities, each probe intensity indicating an extent of hybridization of a nucleic acid probe with said sample sequence, and each nucleic acid probe differing from each other by at least a single base;

said computer system comparing at least one of said plurality of probe intensities with said statistics; and

said computer system generating a base call identifying said unknown base according to results of said comparing step and said sequence of said nucleic acid probe.

100. The method of claim '99, wherein said statistics include a mean and standard deviation.

101. The method of claim 99, further comprising the step of normalizing said plurality of probe intensities by dividing each probe intensity by a sum of related probe intensities, wherein related probe intensities are from probes that differ by a single base.

102. The method of claim 99, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

103. The method of claim 99, further comprising the step of setting a probe intensity equal to a positive number if said probe intensity is less than or equal to zero.

104. The method of claim 99, further comprising the step of indicating said unknown base is unable to be identified if said plurality of probe intensities have insufficient intensity to identify said unknown base.

105. The method of claim 99, wherein said unknown base is identified as being A, C, G, or T.

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1 -- 106. The method of claim 60, wherein the plurality of
2 nucleic acid probes are in an array of probes.

1 107. The method of claim 60, wherein the plurality of
2 probe intensities are fluorescent intensities.

1 108. (Amended) A computer program product that
2 identifies an unknown base in a sample nucleic acid sequence,
3 comprising:

4 computer code that receives a plurality of signals
5 corresponding to probe intensities for a plurality of nucleic
6 acid probes, each probe intensity indicating an extent of
7 hybridization of a nucleic acid probe with at least one nucleic
8 acid sequence including said sample sequence, and each nucleic
9 acid probe differing from each other by at least a single base;

10 computer code that performs a comparison of said
11 plurality of probe intensities to each other;

12 computer code that generates a base call identifying
13 said unknown base according to results of said comparison and
14 said sequences of said nucleic acid probes; and

15 a computer readable medium that stores said computer
16 codes.

1 2109. (Amended) A computer program product that
2 identifies an unknown base in a sample nucleic acid sequence,
3 comprising:

4 computer code that receives a plurality of signals
5 corresponding to probe intensities for a plurality of nucleic
6 acid probes, each probe intensity indicating an extent of
7 hybridization of a nucleic acid probe with said sample sequence,

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8 and each nucleic acid probe differing from each other by at least
9 a single base;

10 computer code that calculates a ratio of a higher probe
11 intensity to a lower probe intensity;

12 computer code that generates a base call identifying
13 said unknown base according to a base of a nucleic acid probe
14 having said higher probe intensity if said ratio is greater than
15 a predetermined ratio value; and

16 a computer readable medium that stores said computer
17 codes.

1 91 3 110. (Amended) A computer program product that
2 identifies an unknown base in a sample nucleic acid sequence,
3 comprising:

4 computer code that receives a first set of signals
5 corresponding to a first set of probe intensities, each probe
6 intensity in said first set indicating an extent of hybridization
7 of a nucleic acid probe with a reference nucleic acid sequence,
8 and each nucleic acid probe differing from each other by at least
9 a single base;

10 computer code that receives a second set of signals
11 corresponding to a second set of probe intensities, each probe
12 intensity in said second set indicating an extent of
13 hybridization of a nucleic acid probe with said sample sequence,
14 and each nucleic acid probe differing from each other by at least
15 a single base;

16 computer code that performs a comparison of at least
17 one of said probe intensities in said first set and at least one
18 of said probe intensities in said second set;

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19 computer code that generates a base call identifying
20 said unknown base according to results of said comparison and
21 said sequence of said nucleic acid probe; and
22 a computer readable medium that stores said computer
23 codes.

1 4 111. (Amended) A computer program product that
2 identifies an unknown base in a sample nucleic acid sequence,
3 comprising:

4 computer code that receives signals corresponding to
5 statistics about a plurality of experiments, each of said
6 experiments producing probe intensities, each probe intensity
7 indicating an extent of hybridization of a nucleic acid probe
8 with a reference nucleic acid sequence, and each nucleic acid
9 probe differing from each other by at least a single base;

10 computer code that receives a plurality of signals
11 corresponding to probe intensities, each probe intensity
12 indicating an extent of hybridization of a nucleic acid probe
13 with said sample sequence, and each nucleic acid probe differing
14 from each other by at least a single base;

15 computer code that performs a comparison of at least
16 one of said plurality of probe intensities with said statistics;

17 computer code that generates a base call identifying
18 said unknown base according to results of said comparison and
19 said sequences of said nucleic acid probes; and

20 a computer readable medium that stores said computer
21 codes.

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1 5 ~~1/2~~. (Amended) A system that identifies an unknown
2 base in a sample nucleic acid sequence, comprising:
3 a processor; and
4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:
6 computer code that receives a plurality of signals
7 corresponding to probe intensities for a plurality of nucleic
8 acid probes, each probe intensity indicating an extent of
9 hybridization of a nucleic acid probe with at least one nucleic
10 acid sequence including said sample sequence, and each nucleic
11 acid probe differing from each other by at least a single base;
12 computer code that performs a comparison of said
13 plurality of probe intensities to each other; and
14 computer code that generates a base call identifying
15 said unknown base according to results of said comparison and
16 said sequences of said nucleic acid probes.

1 6 ~~1/3~~. (Amended) A system that identifies an unknown
2 base in a sample nucleic acid sequence, comprising:
3 a processor; and
4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:
6 computer code that receives a plurality of signals
7 corresponding to probe intensities for a plurality of nucleic
8 acid probes, each probe intensity indicating an extent of
9 hybridization of a nucleic acid probe with said sample sequence,
10 and each nucleic acid probe differing from each other by at least
11 a single base;

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12 computer code that calculates a ratio of a higher probe
13 intensity to a lower probe intensity; and

14 computer code that generates a base call identifying
15 said unknown base according to a base of a nucleic acid probe
16 having said higher probe intensity if said ratio is greater than
17 a predetermined ratio value.

1 7 114. (Amended) A system that identifies an unknown
2 base in a sample nucleic acid sequence, comprising:

3 a processor; and

4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:

6 computer code that receives a first set of signals
7 corresponding to probe intensities, each probe intensity in said
8 first set indicating an extent of hybridization of a nucleic acid
9 probe with a reference nucleic acid sequence, and each nucleic
10 acid probe differing from each other by at least a single base;

11 computer code that receives a second set of signals
12 corresponding to probe intensities, each probe intensity in said
13 second set indicating an extent of hybridization of a nucleic
14 acid probe with said sample sequence, and each nucleic acid probe
15 differing from each other by at least a single base;

16 computer code that performs a comparison of at least
17 one of said probe intensities in said first set and at least one
18 of said probe intensities in said second set; and

19 computer code that generates a base call identifying
20 said unknown base according to results of said comparison and
21 sequence sequences of said
said nucleic acid probe

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1 8 ~~115~~. (Amended) A system that identifies an unknown
2 base in a sample nucleic acid sequence, comprising:

3 a processor; and

4 a computer readable medium coupled to said processor
5 for storing a computer program comprising:

6 computer code that receives signals correponding to
7 statistics about a plurality of experiments, each of said
8 experiments producing probe intensities, each probe intensity
9 indicating an extent of hybridization of a nucleic acid probe
10 with a reference nucleic acid sequence, and each nucleic acid
11 probe differing from each other by at least a single base;

12 computer code that receives a plurality of signals
13 corresponding to probe intensities, each probe intensity
14 indicating an extent of hybridization of a nucleic acid probe
15 with said sample sequence, and each nucleic acid probe differing
16 from each other by at least a single base;

17 computer code that performs a comparison of at least
18 one of said plurality of probe intensities with said statistics;
19 and

20 computer code that generates a base call identifying
21 said unknown base according to results of said comparison and
22 sequence of said
said nucleic acid probes

1 9 ~~116~~. A system according to claims ~~112~~⁵, ~~113~~⁶, ~~114~~⁷, or ~~115~~⁸, wherein the
2 plurality of nucleic acid probes are in an array of probes.

1 10 ~~117~~. A system according to claims ~~112~~⁵, ~~113~~⁶, ~~114~~⁷, or ~~115~~⁸, wherein the
2 plurality of probe intensities are fluorescent intensities.

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